AUG 1 0 2001 65

SEQUENCE LISTING

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Hauptmann, Rudolph Himmler, Adolph Maurer-Fogy, Ingrid Stratowa, Christian

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<223> Portion of TNF-BP pro protein cleaved by extracellular proteases following secretion.

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Glu Ile Ser Ser Cys Thr Val Asp Arg Asp Thr Val Cys Gly Cys Arg
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Gly Thr Thr Val Leu Leu Pro Leu Val Ile Phe Phe Gly Leu Cys Leu 210 215 220

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Arg Asp Thr Val	Cys Gly Cys A	rg Lys Asn Gln Tyr 90	Arg His Tyr Trp 95
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Thr Val His Leu 115		lu\Lys Gln Asn Thr 20	Val Cys Thr Cys 125
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		tat Tyr														953
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Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys Thr Lys Cys His Lys
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Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu Asn His Leu
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Arg His Cys Leu Ser Cys Ser Lys Cys Arg Lys Glu Met Gly Gln Val

Glu Ile Ser Ser Cys Thr Val Asp Arg Asp Thr Val Cys Gly Cys Arg 115 120 125

Lys Asn Gln Tyr Arg His Tyr Trp Set Glu Asn Leu Phe Gln Cys Phe
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Lys Gln Asn Thr Val Cys Thr Cys His Ala Gly Phe Phe Leu Arg Glu 165 170 175

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Lys Leu Cys Leu Pro Gln Ile Glu Asn Val Lys Gly Thr Glu Asp Ser
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Gly Thr Thr Val Leu Leu Pro Leu Val Ile Phe Phe Gly Leu Cys Leu 210 215 220

Leu Ser Leu Leu Phe Ile Gly Leu Met Tyr Arg Tyr Gln Arg Trp Lys 225 230 235 240

Ser Lys Leu Tyr Ser Ile Val Cys Gly Lys Set Thr Pro Glu Lys Glu 245 250 255

Gly Glu Leu Glu Gly Thr Thr Thr Lys Pro Leu Ala Pro Asn Pro Ser 260 265 270

Phe Ser Pro Thr Pro Gly Phe Thr Pro Thr Leu Gly Phe Ser Pro Val

275 280 285 Pro Ser Ser Thr Phe Thr Ser Ser Ser Thr Tyr Thr Pro Gly Asp Cys 295 290 Pro Asn Phe Ala Ala Pro Arg Arg Glu Val Ala Pro Pro Tyr Gln Gly 310 315 Ala Asp Pro Ile Leu Ala Thr\Ala Leu Ala Ser Asp Pro Ile Pro Asn 325 330 Pro Leu Gln Lys Trp Glu Asp Ser Ala His Lys Pro Gln Ser Leu Asp 340 345 Thr Asp Asp Pro Ala Thr Leu Tykr Ala Val Val Glu Asn Val Pro Pro 360 365 Leu Arg Trp 370 <210> 13 <211> 6414 <212> DNA <213> Artificial Sequence <220> <223> Description of Artificial Sequence: pADCMV1 vector <220> <221> unsure <222> (344) <223> "n" can be a, g, c, or t <220> <221> unsure <222> (4157) <223> "n" can be a, g, c, or t <220> <221> unsure <222> (5135) <223> "n" can be a, g, c, or t <220> <221> unsure <222> (6255) <223> "n" can be a, g, c, or t <400> 13 tegacattga ttattgacta gttattaata gtaateaatt åeggggteat tagtteatag 60 cccatatatg gagttccgcg ttacataact tacggtaaat ggcccgcctc gctgaccgcc 120 caacgacccc cgcccattga cgtcaataat gacgtatgtt cccatagtaa cgccaatagg 180

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ctg gct ctg ctg atg ggg ata cac cca tca ggg gtc acc gga ctg gtt Leu Ala Leu Leu Met Gly Ile His Pro Ser Gly Val Thr Gly Leu Val 20 25 30	337
cct tct ctt ggt gac cgg gag aag agg gat aat ttg tgt ccc cag gga Pro Ser Leu Gly Asp Arg Glu Lys Arg Asp Asn Leu Cys Pro Gln Gly 35	385
aag tat gcc cat cca aag aat aat tcc atc tgc tgc acc aag tgc cac Lys Tyr Ala His Pro Lys Asn Asn Ser Ile Cys Cys Thr Lys Cys His 50 55 60	433
aaa gga acc tac ttg gtg agt gac tgt cca agc cca ggg cag gaa aca Lys Gly Thr Tyr Leu Val Ser Asp Cys Pro Ser Pro Gly Gln Glu Thr 65 70 75	481
gtc tgc gag ctc tct cat aaa ggc acc ttt aca gct tcg cag aac cac Val Cys Glu Leu Ser His Lys Gly Thr Phe Thr Ala Ser Gln Asn His 80 85 90 95	529
gtc aga cag tgt ctc agt tgc aag aca tgt cgg aaa gaa atg ttc cag Val Arg Gln Cys Leu Ser Cys Lys Thr Cys Arg Lys Glu Met Phe Gln 100 105 110	577
gtg gag att tct cct tgc aaa gct gac atg gac acc gtg tgt ggc tgc Val Glu Ile Ser Pro Cys Lys Ala Asp Met Asp Thr Val Cys Gly Cys 115 120 125	625
aag aag aac caa ttc cag cgc tac ctg agt gag acg cat ttc cag tgt Lys Lys Asn Gln Phe Gln Arg Tyr Leu Ser Glu Thr His Phe Gln Cys 130 135 140	673
gtg gac tgc agc ccc tgc ttc aat ggc acc gtg aca atc ccc tgt aag Val Asp Cys Ser Pro Cys Phe Asn Gly Thr Val Thr Ile Pro Cys Lys 145 150 155	721
gag aaa cag aac acc gtg tgt aac tgc cac gca gga ttc ttt cta agc Glu Lys Gln Asn Thr Val Cys Asn Cys His Ala Gly Phe Phe Leu Ser 160 165 170 175	769
gga aat gag tgc acc cct tgc agc cac tgc ag aaa aat cag gaa tgt Gly Asn Glu Cys Thr Pro Cys Ser His Cys Lys Asn Gln Glu Cys 180 185 190	817
atg aag ctg tgc cta cct cca gtt gca aat gtc aca aac ccc cag gac Met Lys Leu Cys Leu Pro Pro Val Ala Asn Val Thr Asn Pro Gln Asp 195 200 205	865
tca ggt act gcc gtg ctg ttg cct ctg gtt atc ttc cta ggt ctt tgc Ser Gly Thr Ala Val Leu Leu Pro Leu Val Ile Phe Leu Gly Leu Cys 210 215 220	913

ctt tt Leu Le 22	u Phe			_		_		_	-						961
agg cc Arg Pr 240															1009
gag gt Glu Va															1057
atc cc Ile Pr															1105
agc ac Ser Th	c acc r Thr 290	cca Pro	cgc Arg	ttc Phe	agt Ser	cat His 295	cct	gtc Val	tcc Ser	agt Ser	acc Thr 300	ccc Pro	atc Ile	agc Ser	1153
ccc gt Pro Va	l Phe			-										-	1201
gag gt Glu Va 320															1249
aac cc Asn Pr					_		-				-		-		1297
gcg gc Ala Al	-					_		- 1	-			_	-		1345
gct gt Ala Va		-				_		_	1	_			-		1393
ctc ct Leu Le 38	u Gly														1441
ggg cg Gly Ar 400															1489
cgc cg Arg Ar		_	_			_	-	_	-	1-			-		1537
ctt tg Leu Cy	_	_		_	_		-	-				_			1585
cta ga	a agc	cct	gcc	cac	tcg	tcc	acg	acc	cac	cfc	ccg	cga	taa		1630

Leu Glu Ser Pro Ala His Ser Ser Thr Thr His Leu Pro Arg
450 455 460

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<213> Artificial Sequence

<220>

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Ser Leu Gly Asp Arg Glu Lys Arg Asp Asn Leu Cys Pro Gln Gly Lys
35 40 45

Tyr Ala His Pro Lys Asn Asn Ser Ile Cys Cys Thr Lys Cys His Lys
50 55 60

Gly Thr Tyr Leu Val Ser Asp Cys Pro Ser Pro Gly Gln Glu Thr Val
65 70 75 80

Cys Glu Leu Ser His Lys Gly Thr Phe Thr Ala Ser Gln Asn His Val 85 90 95

Arg Gln Cys Leu Ser Cys Lys Thr Cys Arg Lys\Glu Met Phe Gln Val

Glu Ile Ser Pro Cys Lys Ala Asp Met Asp Thr Val Cys Gly Cys Lys
115 120 125

Lys Asn Gln 130	Phe Gln	Arg Tyr	Leu	Ser	Glu	Thr	His 140	Phe	Gln	Cys	Val
Asp Cys Ser 145	Pro Cys	Phe Asn	Gly	Thr	Val	Thr 155	Ile	Pro	Cys	Lys	Glu 160
Lys Gln Asn	Thr Val 165	Cys Asn	Cys	His	Ala 170	Gly	Phe	Phe	Leu	Ser 175	Gly
Asn Glu Cys	Thr Pro 180	Cys Ser	His	Cys 185	Lys	Lys	Asn	Gln	Glu 190	Cys	Met
Lys Leu Cys 195	Leu Pro	Pro Val	Ala 200	Asn	Val	Thr	Asn	Pro 205	Gln	Asp	Ser
Gly Thr Ala 210	Val Leu	Leu Pro 215	Leu	Val	Ile	Phe	Leu 220	Gly	Leu	Cys	Leu
Leu Phe Phe 225	Ile Cys	Ile Ser 230	Leu	Цеи	Cys	Arg 235	Tyr	Pro	Gln	Trp	Arg 240
Pro Arg Val	Tyr Ser 245	Ile Ile	Cys	Ard	Asp 250	Ser	Ala	Pro	Val	Lys 255	Glu
Val Glu Gly	Glu Gly 260	Ile Val	Thr	Lys 265	Pro	Leu	Thr	Pro	Ala 270	Ser	Ile
Pro Ala Phe 275	Ser Pro	Asn Pro	Gly 280	Phe	Asn	Pro	Thr	Leu 285	Gly	Phe	Ser
Thr Thr Pro 290	Arg Phe	Ser His 295	Pro	Val	Ser	Ser	Thr 300	Pro	Ile	Ser	Pro
Val Phe Gly 305	Pro Ser	Asn Trp 310	His	Asn	Phe	Val 315	Pro	Pro	Val	Arg	Glu 320
Val Val Pro	Thr Gln 325	Gly Ala	Asp	Pro	Leu 330	Leu	Tyr	Gly	Ser	Leu 335	Asn
Pro Val Pro	Ile Pro 340	Ala Pro	Val	Arg 345	Lys	Trb	Glu	Asp	Val 350	Val	Ala
Ala Gln Pro 355	Gln Arg	Leu Asp	Thr 360	Ala	Asp	Pro	Ala	Met 365	Leu	Tyr	Ala
Val Val Asp 370	Gly Val	Pro Pro 375	Thr	Arg	Trp	Lys	Glu 380	Phe	Met	Arg	Leu
Leu Gly Leu 385	Ser Glu	His Glu 390	Ile	Glu	Arg	Leu 395	Glu	Leu	Gln	Asn	Gly 400
Arg Cys Leu	Arg Glu 405	Ala His	Tyr	Ser	Met 410	Leu	Glu	Ala	Trp	Arg 415	Arg
Arg Thr Pro	Arg His 420	Glu Ala	Thr	Leu 425	Asp	Val	Va	Gly	Arg 430	Val	Leu

Cys Asp Met Asn Leu Arg Gly Cys Leu Glu Asn Ile Arg Glu Thr Leu 435 440 445
Glu Ser Pro Ala His Ser Ser Thr Thr His Leu Pro Arg 450 460
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ctggacagac cgagtcccgg gaagccccag dactgccgct gccacactgc cctgagccca 180
katgggggag tgagaggcca tagctgtctg gc atg ggc ctc tcc acc gtg cct 233 Met Gly Leu Ser Thr Val Pro 1 5
gac ctg ctg ctg cca ctg gtg ctc ctg gag ctg ttg gtg gga ata tac 281 Asp Leu Leu Pro Leu Val Leu Leu Glu Leu Leu Val Gly Ile Tyr 10 15 20
ccc tca ggg gtt att gga ctg gtc cct cac cta ggg gac agg gag aag 329 Pro Ser Gly Val Ile Gly Leu Val Pro His Leu Gly Asp Arg Glu Lys 25 30 35
aga gat agt gtg tgt ccc caa gga aaa tat atc cac cct caa aat aat 377 Arg Asp Ser Val Cys Pro Gln Gly Lys Tyr Ile His Pro Gln Asn Asn 40 45 50 55
tcg att tgc tgt acc aag tgc cac aaa gga acc tac ttg tac aat gac 425 Ser Ile Cys Cys Thr Lys Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp 60 65 70
tgt cca ggc ccg ggg cag gat acg gac tgc agg gag tgt gag agc ggc 473 Cys Pro Gly Pro Gly Gln Asp Thr Asp Cys Arg Glu Cys Glu Ser Gly 75 80 85
tcc ttc acc gct tca gaa aac cac ctc aga cac tgc ctc agc tgc tcc 521 Ser'Phe Thr Ala Ser Glu Asn His Leu Arg His Cys Leu Ser Cys Ser 90 95 100
aaa tgc cga aag gaa atg ggt cag gtg gag atc tct tct tgc aca gtg 569 Lys Cys Arg Lys Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr Val

	105			1/10				115			
				ggc Gly							61 ⁷
				cag Gln							665
				tgc Cys							713
				cta Leu							761
				gag Glu 190							809
				gag Glu							857
_	-			ctt Leu	_						905
	_	-		cgg Arg		_	 -				953
				gaa Glu							1001
				aac Asn 270							1049
		_		agt Ser			- 1				1097
				ggt Gly							1145
				tat Tyr							1193
				atc Ile							1241

agc gcc cac aag Ser Ala His Lys 345					1289
tac gcc gtg gtg Tyr Ala Val Val 360					1337
cgg cgc cta ggg Arg Arg Leu Gly				, , ,	1385
aac ggg cgc tgc Asn Gly Arg Cys 395				a Thr Trp	1433
agg cgg cgc acg Arg Arg Arg Thr 410					1481
gtg ctc cgc gac Val Leu Arg Asp 425					1529
gcg ctt tgc ggc Ala Leu Cys Gly 440				_	1577
tga ggctgcgccc c	tgcgggcag c	tctaaggac\cg [.]	teetgega gatege	cttc	1630
caaccccact ttttt	ctgga aagga	ggggt cctgca	gggg caagcaggag	ctagcagccg	1690
cctacttggt gctaa	cccct cgatg	tacat agctit	ctc agctgcctgc	gcgccgccga	1750
cagtcagcgc tgtgc	gcgcg gagag	aggtg cgccg	gggc tcaagagcct	gagtgggtgg	1810
tttgcgagga tgagg	gacgc tatgc	ctcat gcccgt	ttg ggtgtcctca	ccagcaaggc	1870
tgctcggggg cccct	ggttc gtccc	tgagc cttttt	caca gtgcataagc	agttttttt	1930
gtttttgttt tgttt	tgttt tgttt	ttaaa tcaatc	tgt tacactaata	gaaacttggc	1990
actcctgtgc cctct	gcctg gacaa	gcaca tagcaa	ctg aactgtccta	aggcaggggc	2050
gagcacggaa caatg	ggggcc ttcag	ctgga gctgtg	gact tttgtacata	cactaaaatt	2110
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<210> 17

<211> 455

<212> PRT

<213> Artificial Sequence

<220>

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<400> 17 Met Gly Leu Ser Thr 1 5	Val Pro Asp	Leu Leu Leu Pro 10	Leu Val Leu Leu 15
Glu Leu Leu Val Gly	Ile Tyr Pro	Ser Gly Val Ile	Gly Leu Val Pro
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His Leu Gly Asp Arg 35	Glu Lys Arg	Asp Ser Val Cys	Pro Gln Gly Lys 45
Tyr Ile His Pro Gln 50	Asn Asn Ser 55	Ile Cys Cys Thr	Lys Cys His Lys
Gly Thr Tyr Leu Tyr	Asn Asp Cys	Pro Gly Pro Gly	Gln Asp Thr Asp
65		75	80
Cys Arg Glu Cys Glu 85	Ser Gly Ser	Phe Thr Ala Ser	Glu Asn His Leu 95
Arg His Cys Leu Ser 100	Cys Ser Lys	dys Arg Lys Glu 105	Met Gly Gln Val
Glu Ile Ser Ser Cys	Thr Val Asp	Arg Asp Thr Val	Cys Gly Cys Arg
115	120		125
Lys Asn Gln Tyr Arg	His Tyr Trp	Ser Glu Asn Leu	Phe Gln Cys Phe
130	135	140	
Asn Cys Ser Leu Cys	Leu Asn Gly	Thr Val His Leu	Ser Cys Gln Glu
145	150	155	160
Lys Gln Asn Thr Val 165	Cys Thr Cys	His Ala Gly Phe	Phe Leu Arg Glu 175
Asn Glu Cys Val Ser	Cys Ser Asn	Cys Lys Lys Ser	Leu Glu Cys Thr
180		185	190
Lys Leu Cys Leu Pro	Gln Ile Glu	Asn Val Lys Gly	Thr Glu Asp Ser
195	200		205

Gly Glu Leu Glu Gly Thr Thr Thr Lys Pro Leu Ala Pro Asn Pro Ser 260 265 270

Gly Thr Thr Val Leu Leu Pro Leu Val Ile Phe Phe Gly Leu Cys Leu

Leu Ser Leu Leu Phe Ile Gly Leu Met Tyr\Arg Tyr Gln Arg Trp Lys

Ser Lys Leu Tyr Ser Ile Val Cys Gly Lys \$er Thr Pro Glu Lys Glu

Phe Ser Pro Thr Pro Gly Phe Thr Pro Thr Leu Gly Phe Ser Pro Val 275 280 285

Pro Ser Ser Thr Phe Thr Ser Ser Ser Thr Tyr Thr Pro Gly Asp Cys Pro Asn Phe Ala Ala Pro Arg Arg Glu Val Ala Pro Pro Tyr Gln Gly 310 315 Ala Asp Pro Ile Leu Ala Thr Ala Leu Ala Ser Asp Pro Ile Pro Asn 330 Pro Leu Gln Lys Trp Glu Asp Ser Ala His Lys Pro Gln Ser Leu Asp Thr Asp Asp Pro Ala Thr Leu Tyr Ala Val Val Glu Asn Val Pro Pro 355 360 Leu Arg Trp Lys Glu Phe Val Arg Arg Leu Gly Leu Ser Asp His Glu Ile Asp Arg Leu Glu Leu Gln Asn Gly Arg Cys Leu Arg Glu Ala Gln 390 395 Tyr Ser Met Leu Ala Thr Trp Arg Arg Arg Thr Pro Arg Arg Glu Ala 405 Thr Leu Glu Leu Leu Gly Arg Val Leu Arg Asp Met Asp Leu Leu Gly 425 Cys Leu Glu Asp Ile Glu Glu Ala Leu Cys Gly Pro Ala Ala Leu Pro 435 440 Pro Ala Pro Ser Leu Leu Arg 455 <210> 18 <211> 13 <212> PRT <213> Artificial Sequence <220> <223> Description of Artificial Sequence: N-terminal amino acid sequence of protein purified from urine (main sequence) <220> <221> UNSURE <222> (4) <223> Identity of "Xaa" could not be determined. <400> 18 Asp Ser Val Xaa Pro Gln Gly Lys Tyr Ile His Prd Gln 10 <210> 19

<211> 9

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<222> (7)
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<210> 20
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ctacttgtac aatgactgtc caggcccggg gdaggatacg gactgcaggg agtgtgagag 120
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cggctccttc acagcctcag aaaacaacaa g
<210> 21
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<400> 21
Asp Ser Val Cys Pro Gln Gly Lys
<210> 22
<211> 7
<212> PRT
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<222> (1)..(2)
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Xaa Xaa Leu Ser Cys Ser Lys
<210> 23
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<400> 23
Asp Thr Val Cys Gly Cys Arg
<210> 24
<21:1> 11
<212> PRT
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<400> 24
Glu Asn Glu Cys Val Ser Cys Ser Asn Cys Lys
<210> 25
<211> 12
<212> PRT
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<400> 25
Glu Asn Glu Cys Val Ser Cys Ser Asn Cys Lys Lys
<210> 26
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Tyr Ile His Pro Gln Xaa Asn Ser Ile Xaa Xaa Xaa Lys
<210> 27
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<400> 27
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<210> 28
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<400> 28
Leu Val Pro His Leu Gly Asp Arg
<210> 29
<211> 15
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Thr Val Cys Gly
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Gly Xaa Tyr
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Xaa Arg
<210> 35
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<400> 35
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<210> 36
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Ser Leu Glu Cys Thr Lys Leu Cys Leu Pro Gln Ile Glu Asn
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Gln Gly Lys Tyr Ile His Pro	
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<210> 44	

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<210> 45
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<212> DNA
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<400> 45
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<210> 46
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<210> 48
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	20
<210> 51 <211> 20 <212> DNA <213> Artificial Sequence	20
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<210> 53
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<223> Description of Art\ficial Sequence: TNF-BP tryptic cleavage peptide

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<210> 54

<211> 8

<212> PRT

<213> Artificial Sequence

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<400> 54

Phe Thr Ala Ser Glu Asn Asn Lys

<210> 55

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<400> 55

Phe Thr Ala Ser Cys Asn Asn Lys
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<210> 56

<211> 30

<212> DNA

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<223> Description of Artificial Sequence: Hybridization probe

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<223> Description of Artificial Sequence: Hybridization
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<223> Description of Artificial Sequence: Hybridization
     probe
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aaatgtcgga gactcttgtt gttcctaggd
<210> 59
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tgc cac aaa gga acc tac ttg tac aat gad tgt cca ggc ccg ggg cag Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Gln 20 25 30	96
gat acg gac tgc agg gag tgt gag agc ggc tcc ttc aca gcc tca gaa Asp Thr Asp Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu 35	144
aac aac aag gatcc Asn Asn Lys 50	158

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Gln Gly Lys Tyr Ile His Aro Gln Asn Asn Ser Ile Cys Cys Thr Lys
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Cys His Lys Gly Thr Tyr Le\psi Tyr Asn Asp Cys Pro Gly Pro Gly Gln
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Asp Thr Asp Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu
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Asn Asn Lys
     50
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ggtcgacatt gattattgac tag
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